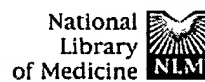


L Number	Hits	Search Text	DB	Time stamp
1	4	TRANSMEMBRANE ADJ TRYPTASE	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/15 09:02

(FILE 'HOME' ENTERED AT 09:10:05 ON 15 DEC 2002)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, CANCERLIT' ENTERED AT 09:10:33 ON
15 DEC 2002

L1 22 S TRANSMEMBRANE TRYPTASE
L2 7 DUP REM L1 (15 DUPLICATES REMOVED)



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#5	Search #4 OR #3	09:14:05	<u>53343</u>
#4	Search TRANSGENIC	09:13:42	<u>35664</u>
#3	Search KNOCKOUT	09:13:34	<u>20741</u>
#2	Related Articles for PubMed (Select 10224463) sort by: PublicationDate	09:13:25	<u>209</u>
#1	Search Wong 118 419	09:12:53	<u>1</u>

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General information about the entry

Entry name	TRYG_MOUSE
Primary accession number	Q9QUL7
Secondary accession numbers	None
Entered in SWISS-PROT in	Release 40, October 2001
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 40, October 2001

Name and origin of the protein

Protein name	Tryptase gamma [Precursor]
Synonyms	EC 3.4.21.- Transmembrane tryptase
Gene name	TPSG1 or TMT
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

References

[1] SEQUENCE FROM NUCLEIC ACID. STRAIN=129/Sv, and BALB/c; MEDLINE=99452974; PubMed=10521469; [NCBI, ExPASy, EBI, Israel, Japan] Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C., Friend D.S., Krilis S.A., Stevens R.L.; "Identification of a new member of the tryptase family of mouse and human mast cell proteases which possesses a novel COOH-terminal hydrophobic extension." J. Biol. Chem. 274:30784-30793(1999).
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Comments

- **SUBCELLULAR LOCATION:** MEMBRANE-ANCHORED (*Potential*).
- **TISSUE SPECIFICITY:** Expressed in many tissues.
- **SIMILARITY:** BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.

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Cross-references

EMBL	AF175760; AAF03698.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF175523; AAF03696.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P20231; 1AAO. [HSSP ENTRY / PDB]
MEROPS	S01.028; -.
MGD	MGI:1349391; Tpsg1.
GeneLynx	TPSG1; Mus musculus.
SOURCE	TPSG1; Mus musculus.
Ensembl	Q9QUL7; Mus musculus. [Entry / Contig view]
	IPR001314; Chymotrypsin.
InterPro	IPR001254; Ser_protease_Try. Graphical view of domain structure.
Pfam	PF00089; trypsin; 1.
PRINTS	PR00722; CHYMOTRYPSIN.
SMART	SM00020; Tryp_SpC; 1.
	PS50240; TRYPSIN_DOM; 1.
PROSITE	PS00134; TRYPSIN_HIS; 1. PS00135; TRYPSIN_SER; FALSE NEG.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	Q9QUL7.
ProtoNet	Q9QUL7.
ProtoMap	Q9QUL7.
PRESAGE	Q9QUL7.
DIP	Q9QUL7.
ModBase	Q9QUL7.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen; Transmembrane.

Features

Key	From	To	Length	Description
SIGNAL	1	16	16	POTENTIAL.
CHAIN	17	28	12	TRYPTASE GAMMA LIGHT CHAIN.
CHAIN	30	311	282	TRYPTASE GAMMA HEAVY CHAIN.
TRANSMEM	277	297	21	POTENTIAL.
ACT_SITE	70	70		CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE	117	117		CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE	214	214		CHARGE RELAY SYSTEM (BY SIMILARITY).
DISULFID	18	137		INTERCHAIN (POTENTIAL).
DISULFID	55	71		BY SIMILARITY.
DISULFID	151	220		BY SIMILARITY.
DISULFID	184	202		BY SIMILARITY.
DISULFID	210	238		BY SIMILARITY.
CARBOHYD	77	77		N-LINKED (GLCNAC...) (POTENTIAL).
CARBOHYD	192	192		N-LINKED (GLCNAC...) (POTENTIAL).



Feature aligner



Feature table viewer

Sequence information

Length: 311 AA [This is the length of the unprocessed precursor] Molecular weight: 32656 Da [This is the MW of the unprocessed precursor] CRC64: 7FC9D6EF6A2A8808 [This is a checksum on the sequence]

```

      10           20           30           40           50           60
MALGPNCGIL LFLAVSGCGH PQVSNVSGSRI VGGHAAPAGT WPWQASLR LH KVVHVC GGSLL

      70           80           90          100          110          120
SPEWVLTA AH CFSGSVNSSD YQVHLGELTV T LSPHFSTVK RIIMYTGSPG PPGSSGDIAL

      130          140          150          160          170          180
VQLSSPVALS SQVQPVCLPE ASADFYPGMQ CWVTGWGYTG EGEPLKPPYN LQEAKVSVVD

      190          200          210          220          230          240
VKTC SQAYNS PNGSLIQPDM LCARGPGDAC QDDSGGPLVC QVAGTWQQAG VVSWGEGCGR

      250          260          270          280          290          300
PDRPGVYARV TAYVNWIIHH IPEAGGSGMQ GLPWAPLLAA LFWPSLFLL VSGVLMAKYW

      310
LSSPSHAASE L

```

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